

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ANDERSON, Darrell R.
HANNA, Nabil
LEONARD, John E.
NEWMAN, Roland A.
REFF, Mitchell E.
RASTETTER, William H.

(ii) TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
LYMPHOMA

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

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(B) STREET: P.O. Box 1404
(C) CITY: Alexandria
(D) STATE: Virginia
(E) COUNTRY: United States
(F) ZIP: 22313-1404

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/149,099
(B) FILING DATE: 03-NOV-1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/978,891
(B) FILING DATE: 12-NOV-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Teskin, Robin L.
(B) REGISTRATION NUMBER: 35,030
(C) REFERENCE/DOCKET NUMBER: 012712-014

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 836-6620
(B) TELEFAX: (703) 836-2021

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGAGCTTGG ATCGATCCTC TATGGTT

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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ATGGTTGCTG ACTAATTGAG ATGCATGCTT TGCATACTTC TGCCTGCTGG GGAGCCTGGG 240
GACTTTCCAC ACCTGGTTGC TGACTAATTG AGATGCATGC TTTGCATACT TCTGCCTGCT 300
GGGGAGCCTG GGGACTTTCC ACACCCTAAC TGACACACAT TCCACAGAAT TAATTCCCCT 360
AGTTATTAAT AGTAATCAAT TACGGGGTCA TTAGTTCATA GCCCATATAT GGAGTTCCGC 420
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TGCCTGCTGA ATAAGTTCTA TCCCAGAGAG GCCAAAGTAC AGTGGAAGGT GGATAACGCC 1200
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 GAATACTCAT ACTCTTCCTT TTTCAATATT ATTGAAGCAT TTATCAGGGT TATTGTCTCA 8460
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 TTCCCCGAAA AGTGCCACCT 8540

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACGTCGCGG CCGCTCTAGG CCTCCAAAA AGCCTCCTCA CTACTTCTGG AATAGCTCAG 60
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GCTGGATCTC	CCGATCCCCA	GCTTTGCTTC	TCAATTTCTT	ATTTGCATAA	TGAGAAAAAA	4200
AGGAAAATTA	ATTTTAACAC	CAATTCAGTA	GTTGATTGAG	CAAATGCGTT	GCCAAAAAGG	4260
ATGCTTTAGA	GACAGTGTTC	TCTGCACAGA	TAAGGACAAA	CATTATTGAG	AGGGAGTACC	4320
CAGAGCTGAG	ACTCCTAAGC	CAGTGAGTGG	CACAGCATTG	TAGGGAGAAA	TATGCTTGTC	4380
ATCACCGAAG	CCTGATTCCG	TAGAGCCACA	CCTTGGTAA	GGCCAATCTG	CTCACACAGG	4440
ATAGAGAGGG	CAGGAGCCAG	GGCAGAGCAT	ATAAGGTGAG	GTAGGATCAG	TTGCTCCTCA	4500
CATTTGCTTC	TGACATAGTT	GTGTTGGGAG	CTTGATAGC	TTGGACAGCT	CAGGGCTGCG	4560
ATTTGCGGCC	AAACTTGACG	GCAATCCTAG	CGTGAAGGCT	GGTAGGATTT	TATCCCCGCT	4620
GCCATCATGG	TTGACCATTT	GAAGTGCATC	GTGCGCGTGT	CCCAAAATAT	GGGGATTGGC	4680

256280-0907250

AAGAACGGAG ACCTACCCTG	CTCCGCTC AGGAACGAGT TCAAGTACTT	AAAGAATG	4740
ACCACAACCT CTTCACTGGA	AGGTAAACAG AATCTGGTGA TTATGGGTAG	GAAAACCTGG	4800
TTCTCCATTG CTGAGAAGAA	TCGACCTTTA AAGGACAGAA TTAATATAGT	TCTCAGTAGA	4860
GAACTCAAAG AACCACCACG	AGGAGCTCAT TTTCTTGCCA AAAGTTTGGA	TGATGCCTTA	4920
AGACTTATTG AACAACCGGA	ATTGGCAAGT AAAGTAGACA TGTTTGGAT	AGTCGGAGGC	4980
AGTTCTGTTT ACCAGGAAGC	CATGAATCAA CCAAGGCCACC TTAGACTCTT	TGTGACAAGG	5040
ATCATGCAGG AATTGAAAG	TGACACGTTT TTCCAGAAA TTGATTGGG	GAAATATAAA	5100
CTTCTCCCAG AATACCCAGG	CGTCCTCTCT GAGGTCCAGG AGGAAAAAGG	CATCAAGTAT	5160
AAGTTTGAAG TCTACGAGAA	GAAAGACTAA CAGGAAGATG CTTTCAAGTT	CTCTGCTCCC	5220
CTCCTAAAGC TATGCATTTT	TATAAGACCA TGGGACTTTT GCTGGCTTTA	GATCAGCCTC	5280
GACTGTGCCT TCTAGTTGCC	AGCCATCTGT TGTGCCCC TCCCCGTGC	CTTCCTTGAC	5340
CCTGGAAGGT GCCACTCCCA	CTGTCTTTT CTAATAAAAT GAGGAAATTG	CATCGCATTG	5400
TCTGAGTAGG TGTCATTCTA	TTCTGGGGGG TGGGTGGGG CAGGACAGCA	AGGGGGAGGA	5460
TTGGGAAGAC AATAGCAGGC	ATGCTGGGGA TCGGTGGGC TCTATGGAAC	CAGCTGGGGC	5520
TCGAGCTACT AGCTTTGCTT	CTCAATTTCT TATTTGCATA ATGAGAAAAA	AAGGAAAAAT	5580
AATTTTAACA CCAATTCAGT	AGTTGATTGA GCAAATGCGT TGCCAAAAAG	GATGCTTTAG	5640
AGACAGTGTT CTCTGCACAG	ATAAGGACAA ACATTATTCA GAGGGAGTAC	CCAGAGCTGA	5700
GACTCCTAAG CCAGTGAGTG	GCACAGCATT CTAGGGAGAA ATATGCTTGT	CATCACCGAA	5760
GCCTGATTCC GTAGAGCCAC	ACCTTGGTAA GGGCCAATCT GCTCACACAG	GATAGAGAGG	5820
GCAGGAGCCA GGGCAGAGCA	TATAAGGTGA GGTAGGATCA GTTGCTCCTC	ACATTTGCTT	5880
CTGACATAGT TGTGTTGGGA	GCTTGGATCG ATCCTCTATG GTTGAACAAG	ATGGATTGCA	5940
CGCAGGTTCT CCGGCCGCTT	GGGTGGAGAG GCTATTCGGC TATGACTGGG	CACAACAGAC	6000
AATCGGCTGC TCTGATGCCG	CCGTGTTCCG GCTGTCAGCG CAGGGGCGCC	CGGTTCTTTT	6060
TGTCAAGACC GACCTGTCCG	GTGCCCTGAA TGAAGTCAG GACGAGGCAG	CGCGGCTATC	6120
GTGGCTGGCC ACGACGGGCG	TTCTTTGCGC AGCTGTGCTC GACGTTGTCA	CTGAAGCGGG	6180
AAGGGACTGG CTGCTATTGG	GCGAAGTGCC GGGGCAGGAT CTCCTGTCAT	CTCACCTTGC	6240
TCCTGCCGAG AAAGTATCCA	TCATGGCTGA TGCAATGCGG CGGCTGCATA	CGCTTGATCC	6300
GGCTACCTGC CCATTGACG	ACCAAGCGAA ACATCGCATC GAGCGAGCAC	GTAATCGGAT	6360
GGAAGCCGGT CTTGTGATC	AGGATGATCT GGACGAAGAG CATCAGGGGC	TCGCGCCAGC	6420
CGAACTGTTT GCCAGGCTCA	AGGCGCGCAT GCGGACGGC GAGGATCTCG	TCGTGACCCA	6480
TGGCGATGCC TGCTTGCCGA	ATATCATGGT GGAAATGGC CGCTTTTCTG	GATTCATCGA	6540
CTGTGGCCCG CTGGGTGTGG	CGGACCGCTA TCAGGACATA GCGTTGGCTA	CCCGTGATAT	6600
TGCTGAAGAG CTTGGCGGCG	AATGGGCTGA CCGCTTCCTC GTGCTTTACG	GTATCGCCGC	6660
TCCCGATTG CAGCGCATCG	CCTTCTATCG CTTCTTGAC GAGTTCTTCT	GAGCGGGACT	6720

CTGGGGTTCG AAATGACCGA AGCGACG CCCAACCTGC CATCACGAGA CGATTCC 6780
 ACCGCCGCCT TCTATGAAAG GTTGGGCTTC GGAATCSTTT TCCGGGACGC CGGCTGGATG 6840
 ATCCTCCAGC GCGGGGATCT CATGCTGGAG TTCTTCGCCC ACCCCAATT GTTTATTGCA 6900
 GCTTATAATG GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTTT 6960
 TCACTGCATT CTAGTTGTGG TTTGTCCAAA CTCATCAATC TATCTTATCA TGTCTGGATC 7020
 GCGGCCGCGA TCCCGTCGAG AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA 7080
 ATTGTTATCC GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAAGCCT 7140
 GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC 7200
 AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG 7260
 GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC 7320
 GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG 7380
 GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCCTAAAA 7440
 AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCC TGACGAGCAT CACAAAAATC 7500
 GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATAACCAG GCGTTTCCCC 7560
 CTGGAAGCTC CCTCGTGCGC TCTCCTGTTT CGACCCTGCC GCTTACCGGA TACCTGTCCG 7620
 CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT 7680
 CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCCGACC 7740
 GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC 7800
 CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG 7860
 AGTTCTTGAA GTGGTGGCCT AACTACGGCT AACTAGAAG GACAGTATTT GGTATCTGCG 7920
 CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA 7980
 CCACCGCTGG TAGCGGTGGT TTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAG 8040
 GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAAT 8100
 CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAGGAT CTTACCTAG ATCCTTTTAA 8160
 ATTAAAAATG AAGTTTTAAA TCAATCTAAA GTATATATGA GTAACTTGG TCTGACAGTT 8220
 ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCTG TCATCCATAG 8280
 TTGCCTGACT CCCCCTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA 8340
 GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTATCA GCAATAAACC 8400
 AGCCAGCCCG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT 8460
 CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG 8520
 TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTGGTATG GCTTCATTCA 8580
 GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG 8640
 TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCACTG TTATCACTCA 8700
 TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG 8760

TGA CTGGTGA GTACTCAACC TCATTCT GAGAATAGTG TATGCGGCGA AGTTGCT 8820
 CTTGCCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA 8880
 TCATTGGAAA AC GTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA 8940
 GTTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG 9000
 TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC 9060
 GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT 9120
 ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGGTTC 9180
 CGCGCACATT TCCCCGAAAA GTGCCACCT 9209

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCACAGATC TCTCACCATG GATTTTCAGG TGCAGATTAT CAGCTTC

47

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGCAGCATCC GTACGTTTGA TTTCCAGCTT

30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: N

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..384

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 67..384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG GAT TTT CAG GTG CAG ATT ATC AGC TTC CTG CTA ATC AGT GCT TCA	48
Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser	
-22 -20 -15 -10	
GTC ATA ATG TCC AGA GGG CAA ATT GTT CTC TCC CAG TCT CCA GCA ATC	96
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile	
-5 -1 1 5 10	
CTG TCT GCA TCT CCA GGG GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC	144
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser	
15 20 25	
TCA AGT GTA AGT TAC ATC CAC TGG TTC CAG CAG AAG CCA GGA TCC TCC	192
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser	
30 35 40	
CCC AAA CCC TGG ATT TAT GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT	240
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro	
45 50 55	
GTT CGC TTC AGT GGC AGT GGG TCT GGG ACT TCT TAC TCT CTC ACA ATC	288
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile	
60 65 70	
AGC AGA GTG GAG GCT GAA GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG	336
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp	
75 80 85 90	
ACT AGT AAC CCA CCC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATC AAA	384
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
95 100 105	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCTCCCA CGCGTGTCTT GTCCCG

27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 3

(D) OTHER INFORMATION: /note= "Nucleotide 3 is N wherein N is G or C."

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 18

(D) OTHER INFORMATION: /note= "Nucleotide 18 is N wherein N is A or C."

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 19

(D) OTHER INFORMATION: /note= "Nucleotide 19 is N wherein N is A or G."

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 25

(D) OTHER INFORMATION: /note= "Nucleotide 25 is N wherein N is G or A."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGNTGTTGTG CTAGCTGNNG AGACNGTGA

29

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..420

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 58..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GGT TGG AGC CTC ATC TTG CTC TTC CTT GTC GCT GTT GCT ACG CGT 48
Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
-19 -15 -10 -5

GTC CTG TCC CAG GTA CAA CTG CAG CAG CCT GGG GCT GAG CTG GTG AAG 96
Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
-1 1 5 10

CCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTT 144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25

ACC AGT TAC AAT ATG CAC TGG GTA AAA CAG ACA CCT GGT CGG GGC CTG 192
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
30 35 40 45

GAA TGG ATT GGA GCT ATT TAT CCC GGA AAT GGT GAT ACT TCC TAC AAT 240
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
50 55 60

CAG AAG TTC AAA GGC AAG GCC ACA TTG ACT GCA GAC AAA TCC TCC AGC 288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
65 70 75

ACA GCC TAC ATG CAG CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC 336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
80 85 90

TAT TAC TGT GCA AGA TCG ACT TAC TAC GGC GGT GAC TGG TAC TTC AAT 384
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
95 100 105

GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCT GCA 420
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
110 115 120